TEAM 4

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION   *US/08/663,618*

DATE: 08/12/96
TIME: 14:23:54

INPUT SET: S12085.raw

> This Raw Listing contains the General
> Information Section and those Sequences
> containing ERRORS.

Does Not Comply
SEQUENCE LISTING**Corrected Diskette Needed**

```
 1
 2
 3    (1)     General Information:
 4
 5        (i) APPLICANT: Gray, Patrick W.
 6
 7       (ii) TITLE OF INVENTION: Chitinase Materials and Methods
 8
 9      (iii) NUMBER OF SEQUENCES: 18      please review this response.
10                                         Many more are shown.
11      (iv) CORRESPONDENCE ADDRESS:
12           (A) ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
13           (B) STREET: 6300 Sears Tower, 233 South Wacker Drive
14           (C) CITY: Chicago
15           (D) STATE: Illinois
16           (E) COUNTRY: United States of America
17           (F) ZIP: 60606-6402
18
19       (v) COMPUTER READABLE FORM:                          See
20           (A) MEDIUM TYPE: Floppy disk                     attached
21           (B) COMPUTER: IBM PC compatible
22           (C) OPERATING SYSTEM: PC-DOS/MS-DOS
23           (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
24
25      (vi) CURRENT APPLICATION DATA:
26           (A) APPLICATION NUMBER:
27           (B) FILING DATE:
28           (C) CLASSIFICATION:
29
30    (viii) ATTORNEY/AGENT INFORMATION:
31           (A) NAME: Rin-Laures, Li-Hsien
32           (B) REGISTRATION NUMBER: 33,547
33           (C) REFERENCE/DOCKET NUMBER: 27866/32960
34
35      (ix) TELECOMMUNICATION INFORMATION:
36           (A) TELEPHONE: 312/474-6300
37           (B) TELEFAX: 312/474-0448
38           (C) TELEX: 25-3856
39
```

ERRORED SEQUENCES FOLLOW:

INPUT SET: S12085.raw

```
40   (2) INFORMATION FOR SEQ ID NO:1:
41
42        (i) SEQUENCE CHARACTERISTICS:
43            (A) LENGTH: 1636 base pairs          last line reads 1645?
44            (B) TYPE: nucleic acid
45            (C) STRANDEDNESS: single
46            (D) TOPOLOGY: linear
47
48        (ii) MOLECULE TYPE: cDNA
49
50        (ix) FEATURE:
51            (A) NAME/KEY: CDS
52            (B) LOCATION: 2..1399
53
54        (ix) FEATURE:
55            (A) NAME/KEY: mat_peptide          Also see
56            (B) LOCATION: 65..1399               error
57                                                  here
58        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
59
60   C ATG GTG CGG TCT GTG GCC TGG GCA GGT TTC ATG GTC CTG CTG ATG        46
61     Met Val Arg Ser Val Ala Trp Ala Gly Phe Met Val Leu Leu Met
62     -21 -20              -15                 -10
63
64   ATC CCA TGG GGC TCT GCT GCA AAA CTG GTC TGC TAC TTC ACC AAC TGG      94
65   Ile Pro Trp Gly Ser Ala Ala Lys Leu Val Cys Tyr Phe Thr Asn Trp
66        -5               1               5                    10
67
68   GCC CAG TAC AGA CAG GGG GAG GCT CGC TTC CTG CCC AAG GAC TTG GAC      142
69   Ala Gln Tyr Arg Gln Gly Glu Ala Arg Phe Leu Pro Lys Asp Leu Asp
70                15                  20                  25
71
72   CCC AGC CTT TGC ACC CAC CTC ATC TAC GCC TTC GCT GGC ATG ACC AAC     190
73   Pro Ser Leu Cys Thr His Leu Ile Tyr Ala Phe Ala Gly Met Thr Asn
74                30                  35                  40
75
76   CAC CAG CTG AGC ACC ACT GAG TGG AAT GAC GAG ACT CTC TAC CAG GAG     238
77   His Gln Leu Ser Thr Thr Glu Trp Asn Asp Glu Thr Leu Tyr Gln Glu
78                45                  50                  55
79
80   TTC AAT GGC CTG AAG AAG ATG AAT CCC AAG CTG AAG ACC CTG TTA GCC     286
81   Phe Asn Gly Leu Lys Lys Met Asn Pro Lys Leu Lys Thr Leu Leu Ala
82        60                  65                  70
83
84   ATC GGA GGC TGG AAT TTC GGC ACT CAG AAG TTC ACA GAT ATG GTA GCC     334
85   Ile Gly G GTTT CCCTGCTGAA TGCCTCGCTC          900
86
87   CCTTCAAGAC GAGGGGCAGG GAAGGACAGG ACCCTCAGGA ATTCAGTGCC TTCAACAACG    960
88
89   TGAGAGAAAG AGAGAAGCCA GCCACAGACC CCTGGGAGCT TCCGCTTTGA AAGAAGCAAG   1020
90
91   ACACGTGGCC TCGTGAGGGG CAAGCTAGGC CCCAGAGGCC CTGGAGGTCT CCAGGGGCCT   1080
92
```

big
jump
in
numbers

INPUT SET: S12085.raw

```
 93    GCAGAAGGAA AGAAGGGGGC CCTGCTACCT GTTCTTGGGC CTCAGGCTCT GCACAGACAA    1140
 94
 95    GCAGCCCTTG CTTTCGGAGC TCCTGTCCAA AGTAGGGATG CGGATCCTGC TGGGGCCGCC    1200
 96
 97    ACGGCCTGGT GGTGGGAAGG CCGGCAGCGG GCGGAGGGGA TCCAGCCACT TCCCCCTCTT    1260
 98
 99    CTTCTGAAGA TCAGAACATT CAGCTCTGGA GAACAGTGGT TGCCTGGGGG CTTTTGCCAC    1320
100
101    TCCTTGTCCC CCGTGATCTC CCCTCACACT TTGCCATTTG CTTGTACTGG GACATTGTTC    1380
102
103    TTTCCGGCCG AGGTGCCACC ACCCTGCCCC CACTAAGAGA CACATACAGA GTGGGCCCCG    1440
104
105    GGCTGGAGAA AGAGCTGCCT GGATGAGAAA CAGCTCAGCC AGTGGGGATG AGGTCACCAG    1500
106
107    GGGAGGAGCC TGTGCGTCCC AGCTGAAGGC AGTGGCAGGG GAGCAGGTTC CCCAAGGGCC    1560
108
109    CTGGCACCCC CACAAGCTGT CCCTGCAGGG CCATCTGACT GCCAAGCCAG ATTCTCTTGA    1620
110
111    ATAAAGTATT CTAGTGTGGA AACGC                                          1645
112
```

```
257    (2) INFORMATION FOR SEQ ID NO:8:
258
259        (i) SEQUENCE CHARACTERISTICS:
260            (A) LENGTH: 170 base pairs
261            (B) TYPE: nucleic acid
262            (C) STRANDEDNESS: single
263            (D) TOPOLOGY: unknown
264
265
266
267        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
268
269        Met Pro Val Met Arg Leu Phe Pro Cys Phe Leu Gln Leu Leu Ala Gly
270        1               5                   10                  15
271
272        Leu Ala Leu Pro Ala Val Pro Pro Gln Gln Trp Ala Leu Ser Ala Gly
273                      20                  25                  30
274
275        Asn Gly Ser Ser Glu Val Glu Val Val Pro Phe Gln Glu Val Trp Gly
276                  35                  40                  45
277
278        Arg Ser Tyr Cys Arg Ala Leu Glu Arg Leu Val Asp Val Val Ser Glu
279              50                  55                  60
280
281        Tyr Pro Ser Glu Val Glu His Met Phe Ser Pro Ser Cys Val Ser Leu
282        65                  70                  75                  80
283
284        Leu Arg Cys Thr Gly Cys Cys Gly Asp Glu Asn Leu His Cys Val Pro
285                      85                  90                  95
286
287        Val Glu Thr Ala Asn Val Thr Met Gln Leu Leu Lys Ile Arg Ser Gly
288                      100                 105                 110
```

[handwritten annotations:] only 169 shown, See more detail in attached pages

```
289
290        Asp Arg Pro Ser Tyr Val Glu Leu Thr Phe Ser Gln His Val Arg Cys
291             115                 120                 125
292
293        Glu Cys Arg Pro Leu Arg Glu Lys Met Lys Pro Glu Arg Arg Arg Pro
294             130                 135                 140
295
296        Lys Gly Arg Gly Lys Arg Arg Arg Glu Lys Gln Arg Pro Thr Asp Cys
297             145                 150                 155
298
299        His Leu Cys Gly Asp Ala Val Pro Arg Arg     ←— 169
300             160                 165
301    (i) SEQUENCE CHARACTERISTICS:
302            (A) LENGTH: 12 amino acids
303            (B) TYPE: amino acid
304            (C) STRANDEDNESS: single
305            (D) TOPOLOGY: linear
306
307    (ii) MOLECULE TYPE: peptide
308
--> 309    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:
310
311        Trp Arg Lys Phe Ala Leu Leu Gly Ser Gly Pro Thr
312        1                   5                   10
313
314
```

```
--> 315    (2) INFORMATION FOR SEQ ID NO:159:
316
317        (i) SEQUENCE CHARACTERISTICS:
318            (A) LENGTH: 12 amino acids
319            (B) TYPE: amino acid
320            (C) STRANDEDNESS: single
321            (D) TOPOLOGY: linear
322
323    (ii) MOLECULE TYPE: peptide
324
325    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:
326
327        His Arg Ala Tyr Arg Ile Ala Thr Met Phe Ser Gly
328        1                   5                   10
329
330
```

See next page

```
363    (2) INFORMATION FOR SEQ ID NO:162:
364
365        (i) SEQUENCE CHARACTERISTICS:
366            (A) LENGTH: 12 amino acids
367            (B) TYPE: amino acid
368            (C) STRANDEDNESS: single
369            (D) TOPOLOGY: linear
370
371    (ii) MOLECULE TYPE: peptide
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```
Met Pro Val Met Arg Leu Phe Pro Cys Phe Leu Gln Leu Leu Ala Gly
1               5                   10                  15

Leu Ala Leu Pro Ala Val Pro Pro Gln Gln Trp Ala Leu Ser Ala Gly
                20          25                  30

Asn Gly Ser Ser Glu Val Glu Val Val Pro Phe Gln Glu Val Trp Gly
            35              40                  45

Arg Ser Tyr Cys Arg Ala Leu Glu Arg Leu Val Asp Val Val Ser Glu
        50              55              60

Tyr Pro Ser Glu Val Glu His Met Phe Ser Pro Ser Cys Val Ser Leu
65              70                  75                      80

Leu Arg Cys Thr Gly Cys Cys Gly Asp Glu Asn Leu His Cys Val Pro
                85              90                  95

Val Glu Thr Ala Asn Val Thr Met Gln Leu Leu Lys Ile Arg Ser Gly
            100             105             110

Asp Arg Pro Ser Tyr Val Glu Leu Thr Phe Ser Gln His Val Arg Cys
            115             120                 125

Glu Cys Arg Pro Leu Arg Glu Lys Met Lys Pro Glu Arg Arg Arg Pro
    130             135                 140

Lys Gly Arg Gly Lys Arg Arg Arg Glu Lys Gln Arg Pro Thr Asp Cys
    145                 150                 155

His Leu Cys Gly Asp Ala Val Pro Arg Arg
160                 165
```

(i) SEQUENCE CHARACTERISTICS: ⟵ *main heading missing.*
        (A) LENGTH: 12 amino acids   *Also, this jumps from*
        (B) TYPE: amino acid   *Seq-8 to 158?*
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

```
Trp Arg Lys Phe Ala Leu Leu Gly Ser Gly Pro Thr
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:159:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 12 amino acids
            (B) TYPE: amino acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

```
His Arg Ala Tyr Arg Ile Ala Thr Met Phe Ser Gly
1               5               10
```

(2) INFORMATION FOR SEQ ID NO:160:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 11 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

```
Arg Gly Leu Met Arg Arg Ser Thr Lys Thr Val
1               5               10
```

(2) INFORMATION FOR SEQ ID NO:161:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 12 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

```
Ala Arg His Arg Met Phe Gln Trp Ala Met Val Gly
1               5               10
```

(2) INFORMATION FOR SEQ ID NO:162:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 12 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: peptide

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Ile Met Ile Gly Lys Glu Gly Ala Val Ser Ser Ser
1   5   10

(2) INFORMATION FOR SEQ ID NO:24:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 12 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

   (vii) IMMEDIATE SOURCE:
        (B) CLONE: 73 2 0.5

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Trp Gln Asn Arg Thr His Lys Val Val Ser Gly Arg
1   5   10

(2) INFORMATION FOR SEQ ID NO:25:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 7 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

   (vii) IMMEDIATE SOURCE:
        (B) CLONE: 78 2 1.1

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Ala Arg Lys His Lys Val Thr
1   5

(2) INFORMATION FOR SEQ ID NO:26:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 11 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

   (vii) IMMEDIATE SOURCE:
        (B) CLONE: 40 3 1.1

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Arg Gln Val Thr Arg Leu His Lys Val Ile His
1   5   10

Now it is back to seq. 24?? & continues on to seq. 70